



SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: Tryggvason, Karl  
Kallunki, Pekka  
Pyke, Charles
- (ii) TITLE OF INVENTION: Laminin Chains: Diagnostic Uses
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fay Sharpe Fagan Minnich & McKee
  - (B) STREET: 1100 Superior Ave, Suite 700
  - (C) CITY: Cleveland
  - (D) STATE: Ohio
  - (E) COUNTRY: USA
  - (F) ZIP: 44114
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Unknown
  - (B) FILING DATE: 08 January 2001
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/663,147
  - (B) FILING DATE: 150-September 2000
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Minnich, Richard, J.
  - (B) REGISTRATION NUMBER: 24,175
  - (C) REFERENCE/DOCKET NUMBER: TRV 20014
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 216-861-5582
  - (B) TELEFAX: 216-241-1666

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligomer primers"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATCACTGA GCAGCTGAAC

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGTACCAGA ACCGAGTTTCG

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGTTACCA GGCTTGAGAG

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTACTGCGGA ATCTCACAGC

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACACTGTTC AACCCAGGGT

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAACAAGCCC TCTCACTGGT

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGGAGACTG TGCTGATAAG

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATACCTCTC TACATGGCAT

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGTCTCGCTG AATCTCTCTT

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTACAACTAG CATGGTGCCC

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 118..183

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 118..3699

(ix) FEATURE:

- (A) NAME/KEY: polyA\_site
- (B) LOCATION: 4433

(ix) FEATURE:

- (A) NAME/KEY: polyA\_site
- (B) LOCATION: 5195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACCACCTGA TCGAAGGAAA AGGAAGGCAC AGCGGAGCGC AGAGTGAGAA CCACCAACCG	60
AGGCGCCGGG CAGCGACCCC TGCAGCGGAG ACAGAGACTG AGCGGCCCCG CACCGCC	117
ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu 1 5 10 15	165
CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly 20 25 30	213
AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly 35 40 45	261
AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His 50 55 60	309
TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg 65 70 75 80	357
TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys 85 90 95	405
GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg 100 105 110	453
TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys 115 120 125	501
ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala 130 135 140	549
GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala 145 150 155 160	597
GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu 165 170 175	645
GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His 180 185 190	693
TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr 195 200 205	741
TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn	789

210	215	220	
GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe 225 230 235 240			837
AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys 245 250 255			885
TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp 260 265 270			933
TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile 275 280 285			981
CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly 290 295 300			1029
AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn 305 310 315 320			1077
GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr 325 330 335			1125
CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr 340 345 350			1173
GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala 355 360 365			1221
CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys 370 375 380			1269
CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr 385 390 395 400			1317
AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys 405 410 415			1365
AAC TGT CAA GGG GGA GGG GCC TGT GAT CCA GAC ACA GGA GAT TGT TAT Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr 420 425 430			1413
TCA GGG GAT GAG AAT CCT GAC ATT GAG TGT GCT GAC TGC CCA ATT GGT Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly 435 440 445			1461
TTC TAC AAC GAT CCG CAC GAC CCC CGC AGC TGC AAG CCA TGT CCC TGT			1509

Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys		
450						455					460						
CAT	AAC	GGG	TTC	AGC	TGC	TCA	GTG	ATT	CCG	GAG	ACG	GAG	GAG	GTG	GTG	1557	
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Ile	Pro	Glu	Thr	Glu	Glu	Val	Val		
465					470					475					480		
TGC	AAT	AAC	TGC	CCT	CCC	GGG	GTC	ACC	GGT	GCC	CGC	TGT	GAG	CTC	TGT	1605	
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys		
				485					490					495			
GCT	GAT	GGC	TAC	TTT	GGG	GAC	CCC	TTT	GGT	GAA	CAT	GGC	CCA	GTG	AGG	1653	
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg		
			500					505					510				
CCT	TGT	CAG	CCC	TGT	CAA	TGC	AAC	AGC	AAT	GTG	GAC	CCC	AGT	GCC	TCT	1701	
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Ser	Asn	Val	Asp	Pro	Ser	Ala	Ser		
		515					520					525					
GGG	AAT	TGT	GAC	CGG	CTG	ACA	GGC	AGG	TGT	TTG	AAG	TGT	ATC	CAC	AAC	1749	
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn		
	530					535					540						
ACA	GCC	GGC	ATC	TAC	TGC	GAC	CAG	TGC	AAA	GCA	GGC	TAC	TTC	GGG	GAC	1797	
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp		
545					550					555					560		
CCA	TTG	GCT	CCC	AAC	CCA	GCA	GAC	AAG	TGT	CGA	GCT	TGC	AAC	TGT	AAC	1845	
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn		
				565					570					575			
CCC	ATG	GGC	TCA	GAG	CCT	GTA	GGA	TGT	CGA	AGT	GAT	GGC	ACC	TGT	GTT	1893	
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys	Val		
			580					585					590				
TGC	AAG	CCA	GGA	TTT	GGT	GGC	CCC	AAC	TGT	GAG	CAT	GGA	GCA	TTC	AGC	1941	
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe	Ser		
		595					600					605					
TGT	CCA	GCT	TGC	TAT	AAT	CAA	GTG	AAG	ATT	CAG	ATG	GAT	CAG	TTT	ATG	1989	
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe	Met		
	610					615					620						
CAG	CAG	CTT	CAG	AGA	ATG	GAG	GCC	CTG	ATT	TCA	AAG	GCT	CAG	GGT	GGT	2037	
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly	Gly		
625					630					635					640		
GAT	GGA	GTA	GTA	CCT	GAT	ACA	GAG	CTG	GAA	GGC	AGG	ATG	CAG	CAG	GCT	2085	
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Glu	Gly	Arg	Met	Gln	Gln	Ala		
				645					650					655			
GAG	CAG	GCC	CTT	CAG	GAC	ATT	CTG	AGA	GAT	GCC	CAG	ATT	TCA	GAA	GGT	2133	
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu	Gly		
			660					665					670				
GCT	AGC	AGA	TCC	CTT	GGT	CTC	CAG	TTG	GCC	AAG	GTG	AGG	AGC	CAA	GAG	2181	
Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu		
		675					680						685				

AAC AGC TAC CAG AGC CGC CTG GAT GAC CTC AAG ATG ACT GTG GAA AGA Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg 690 695 700	2229
GTT CGG GCT CTG GGA AGT CAG TAC CAG AAC CGA GTT CGG GAT ACT CAC Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His 705 710 715 720	2277
AGG CTC ATC ACT CAG ATG CAG CTG AGC CTG GCA GAA AGT GAA GCT TCC Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser 725 730 735	2325
TTG GGA AAC ACT AAC ATT CCT GCC TCA GAC CAC TAC GTG GGG CCA AAT Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn 740 745 750	2373
GGC TTT AAA AGT CTG GCT CAG GAG GCC ACA AGA TTA GCA GAA AGC CAC Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His 755 760 765	2421
GTT GAG TCA GCC AGT AAC ATG GAG CAA CTG ACA AGG GAA ACT GAG GAC Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp 770 775 780	2469
TAT TCC AAA CAA GCC CTC TCA CTG GTG CGC AAG GCC CTG CAT GAA GGA Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly 785 790 795 800	2517
GTC GGA AGC GGA AGC GGT AGC CCG GAC GGT GCT GTG GTG CAA GGG CTT Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu 805 810 815	2565
GTG GAA AAA TTG GAG AAA ACC AAG TCC CTG GCC CAG CAG TTG ACA AGG Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg 820 825 830	2613
GAG GCC ACT CAA GCG GAA ATT GAA GCA GAT AGG TCT TAT CAG CAC AGT Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser 835 840 845	2661
CTC CGC CTC CTG GAT TCA GTG TCT CCG CTT CAG GGA GTC AGT GAT CAG Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln 850 855 860	2709
TCC TTT CAG GTG GAA GAA GCA AAG AGG ATC AAA CAA AAA GCG GAT TCA Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser 865 870 875 880	2757
CTC TCA AGC CTG GTA ACC AGG CAT ATG GAT GAG TTC AAG CGT ACA CAA Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln 885 890 895	2805
AAG AAT CTG GGA AAC TGG AAA GAA GAA GCA CAG CAG CTC TTA CAG AAT Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn 900 905 910	2853
GGA AAA AGT GGG AGA GAG AAA TCA GAT CAG CTG CTT TCC CGT GCC AAT Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn	2901



915	920	925	
CTT GCT AAA AGC AGA GCA CAA GAA GCA CTG AGT ATG GGC AAT GCC ACT Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr 930 935 940			2949
TTT TAT GAA GTT GAG AGC ATC CTT AAA AAC CTC AGA GAG TTT GAC CTG Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu 945 950 955 960			2997
CAG GTG GAC AAC AGA AAA GCA GAA GCT GAA GAA GCC ATG AAG AGA CTC Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu 965 970 975			3045
TCC TAC ATC AGC CAG AAG GTT TCA GAT GCC AGT GAC AAG ACC CAG CAA Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln 980 985 990			3093
GCA GAA AGA GCC CTG GGG AGC GCT GCT GCT GAT GCA CAG AGG GCA AAG Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys 995 1000 1005			3141
AAT GGG GCC GGG GAG GCC CTG GAA ATC TCC AGT GAG ATT GAA CAG GAG Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu 1010 1015 1020			3189
ATT GGG AGT CTG AAC TTG GAA GCC AAT GTG ACA GCA GAT GGA GCC TTG Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu 1025 1030 1035 1040			3237
GCC ATG GAA AAG GGA CTG GCC TCT CTG AAG AGT GAG ATG AGG GAA GTG Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val 1045 1050 1055			3285
GAA GGA GAG CTG GAA AGG AAG GAG CTG GAG TTT GAC ACG AAT ATG GAT Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp 1060 1065 1070			3333
GCA GTA CAG ATG GTG ATT ACA GAA GCC CAG AAG GTT GAT ACC AGA GCC Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala 1075 1080 1085			3381
AAG AAC GCT GGG GTT ACA ATC CAA GAC ACA CTC AAC ACA TTA GAC GGC Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly 1090 1095 1100			3429
CTC CTG CAT CTG ATG GAC CAG CCT CTC AGT GTA GAT GAA GAG GGG CTG Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu 1105 1110 1115 1120			3477
GTC TTA CTG GAG CAG AAG CTT TCC CGA GCC AAG ACC CAG ATC AAC AGC Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser 1125 1130 1135			3525
CAA CTG CGG CCC ATG ATG TCA GAG CTG GAA GAG AGG GCA CGT CAG CAG Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln 1140 1145 1150			3573

AGG GGC CAC CTC CAT TTG CTG GAG ACA AGC ATA GAT GGG ATT CTG GCT	3621
Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala	
1155 1160 1165	
GAT GTG AAG AAC TTG GAG AAC ATT AGG GAC AAC CTG CCC CCA GGC TGC	3669
Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys	
1170 1175 1180	
TAC AAT ACC CAG GCT CTT GAG CAA CAG TGA AGCTGCCATA AATATTTCTC	3719
Tyr Asn Thr Gln Ala Leu Glu Gln Gln *	
1185 1190	
AACTGAGGTT CTTGGGATAC AGATCTCAGG GCTCGGGAGC CATGTCATGT GAGTGGGTGG	3779
GATGGGGACA TTTGAACATG TTTAATGGGT ATGCTCAGGT CAACTGACCT GACCCCATTC	3839
CTGATCCCAT GGCCAGGTGG TTGTCTTATT GCACCATACT CCTTGCTTCC TGATGCTGGG	3899
CATGAGGCAG ATAGGCACTG GTGTGAGAAT GATCAAGGAT CTGGACCCCA AAGATAGACT	3959
GGATGGAAAG ACAAACTGCA CAGGCAGATG TTTGCCTCAT AATAGTCGTA AGTGGAGTCC	4019
TGGAATTTGG ACAAGTGCTG TTGGGATATA GTCAACTTAT TCTTTGAGTA ATGTGACTAA	4079
AGGAAAAAAC TTTGACTTTG CCCAGGCATG AAATTCTTCC TAATGTCAGA ACAGAGTGCA	4139
ACCCAGTCAC ACTGTGGCCA GTAAAATACT ATTGCCTCAT ATTGTCCTCT GCAAGCTTCT	4199
TGCTGATCAG AGTTCCTCCT ACTTACAACC CAGGGTGTGA ACATGTTCTC CATTTTCAAG	4259
CTGGAAGAAG TGAGCAGTGT TGGAGTGAGG ACCTGTAAGG CAGGCCCATT CAGAGCTATG	4319
GTGCTTGCTG GTGCCTGCCA CCTTCAAGTT CTGGACCTGG GCATGACATC CTTTCTTTTA	4379
ATGATGCCAT GGCAACTTAG AGATTGCATT TTTATTAAAG CATTTCTTAC CAGCAAAGCA	4439
AATGTTGGGA AAGTATTTAC TTTTTCGGTT TCAAAGTGAT AGAAAAGTGT GGCTTGGGCA	4499
TTGAAAGAGG TAAAATTCTC TAGATTTATT AGTCCTAATT CAATCCTACT TTTCGAACAC	4559
CAAAAATGAT GCGCATCAAT GTATTTTATC TTATTTTCTC AATCTCCTCT CTCTTTCCTC	4619
CACCCATAAT AAGAGAATGT TCCTACTCAC ACTTCAGCTG GGTACATCC ATCCCTCCAT	4679
TCATCCTTCC ATCCATCTTT CCATCCATTA CCTCCATCCA TCCTTCCAAC ATATATTTAT	4739
TGAGTACCTA CTGTGTGCCA GGGGCTGGTG GGACAGTGGT GACATAGTCT CTGCCCTCAT	4799
AGAGTTGATT GTCTAGTGAG GAAGACAAGC ATTTTAAAAA AATAAATTTA AACTTACAAA	4859
CTTTGTTTGT CACAAGTGGT GTTTATTGCA ATAACCGCTT GGTTTGCAAC CTCTTGCTC	4919
AACAGAACAT ATGTTGCAAG ACCCTCCCAT GGGCACTGAG TTTGGCAAGG ATGACAGAGC	4979
TCTGGGTTGT GCACATTTCT TTGCATTCCA GCGTCACTCT GTGCCTTCTA CAACTGATTG	5039
CAACAGACTG TTGAGTTATG ATAACACCAG TGGGAATTGC TGGAGGAACC AGAGGCACTT	5099
CCACCTTGGC TGGGAAGACT ATGGTGCTGC CTTGCTTCTG TATTCCTTG GATTTTCCTG	5159

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
 1             5             10             15

Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
 20             25             30

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
 35             40             45

Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
 50             55             60

Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
 65             70             75             80

Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
 85             90             95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
100            105            110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
115            120            125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
130            135            140

Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145            150            155            160

Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
165            170            175

Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
180            185            190

Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
195            200            205

Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
210            215            220

Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225            230            235            240

Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys

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245								250					255			
Phe	Leu	Gly	Asn	Gln	Gln	Val	Ser	Tyr	Gly	Gln	Ser	Leu	Ser	Phe	Asp	
			260				265						270			
Tyr	Arg	Val	Asp	Arg	Gly	Gly	Arg	His	Pro	Ser	Ala	His	Asp	Val	Ile	
			275				280						285			
Leu	Glu	Gly	Ala	Gly	Leu	Arg	Ile	Thr	Ala	Pro	Leu	Met	Pro	Leu	Gly	
			290				295						300			
Lys	Thr	Leu	Pro	Cys	Gly	Leu	Thr	Lys	Thr	Tyr	Thr	Phe	Arg	Leu	Asn	
305			310						315			320				
Glu	His	Pro	Ser	Asn	Asn	Trp	Ser	Pro	Gln	Leu	Ser	Tyr	Phe	Glu	Tyr	
			325						330			335				
Arg	Arg	Leu	Leu	Arg	Asn	Leu	Thr	Ala	Leu	Arg	Ile	Arg	Ala	Thr	Tyr	
			340			345						350				
Gly	Glu	Tyr	Ser	Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Ile	Ser	Ala	
			355			360						365				
Arg	Pro	Val	Ser	Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Gln	Cys	Ile	Cys	
370			375						380							
Pro	Val	Gly	Tyr	Lys	Gly	Gln	Phe	Cys	Gln	Asp	Cys	Ala	Ser	Gly	Tyr	
385			390						395			400				
Lys	Arg	Asp	Ser	Ala	Arg	Leu	Gly	Pro	Phe	Gly	Thr	Cys	Ile	Pro	Cys	
			405			410						415				
Asn	Cys	Gln	Gly	Gly	Gly	Ala	Cys	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Tyr	
			420			425						430				
Ser	Gly	Asp	Glu	Asn	Pro	Asp	Ile	Glu	Cys	Ala	Asp	Cys	Pro	Ile	Gly	
			435			440						445				
Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys	
450			455						460							
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Ile	Pro	Glu	Thr	Glu	Glu	Val	Val	
465			470						475			480				
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys	
			485			490						495				
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg	
			500			505						510				
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Ser	Asn	Val	Asp	Pro	Ser	Ala	Ser	
515			520						525							
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn	
530			535						540							
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp	
545			550			555						560				
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn	

565					570					575					
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys	Val
			580					585					590		
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe	Ser
		595					600					605			
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe	Met
	610					615					620				
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly	Gly
625					630					635					640
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Glu	Gly	Arg	Met	Gln	Gln	Ala
				645					650						655
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu	Gly
			660					665						670	
Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu
		675					680					685			
Asn	Ser	Tyr	Gln	Ser	Arg	Leu	Asp	Asp	Leu	Lys	Met	Thr	Val	Glu	Arg
	690					695					700				
Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Arg	Val	Arg	Asp	Thr	His
705						710					715				720
Arg	Leu	Ile	Thr	Gln	Met	Gln	Leu	Ser	Leu	Ala	Glu	Ser	Glu	Ala	Ser
				725					730					735	
Leu	Gly	Asn	Thr	Asn	Ile	Pro	Ala	Ser	Asp	His	Tyr	Val	Gly	Pro	Asn
			740					745					750		
Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Leu	Ala	Glu	Ser	His
		755					760					765			
Val	Glu	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Thr	Arg	Glu	Thr	Glu	Asp
	770					775					780				
Tyr	Ser	Lys	Gln	Ala	Leu	Ser	Leu	Val	Arg	Lys	Ala	Leu	His	Glu	Gly
785						790					795				800
Val	Gly	Ser	Gly	Ser	Gly	Ser	Pro	Asp	Gly	Ala	Val	Val	Gln	Gly	Leu
				805					810					815	
Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg
			820					825					830		
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser
			835				840					845			
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Pro	Leu	Gln	Gly	Val	Ser	Asp	Gln
	850					855					860				
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser
865						870					875				880
Leu	Ser	Ser	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln

885					890					895					
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn
			900						905					910	
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn
			915					920					925		
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr
			930					935					940		
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu
									950					955	960
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu
									965					970	975
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln
									980					985	990
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys
									995					1000	1005
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu
									1010					1015	1020
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu
									1025					1030	1035
Ala	Met	Glu	Lys	Gly	Leu	Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val
									1045					1050	1055
Glu	Gly	Glu	Leu	Glu	Arg	Lys	Glu	Leu	Glu	Phe	Asp	Thr	Asn	Met	Asp
									1060					1065	1070
Ala	Val	Gln	Met	Val	Ile	Thr	Glu	Ala	Gln	Lys	Val	Asp	Thr	Arg	Ala
									1075					1080	1085
Lys	Asn	Ala	Gly	Val	Thr	Ile	Gln	Asp	Thr	Leu	Asn	Thr	Leu	Asp	Gly
									1090					1095	1100
Leu	Leu	His	Leu	Met	Asp	Gln	Pro	Leu	Ser	Val	Asp	Glu	Glu	Gly	Leu
									1105					1110	1115
Val	Leu	Leu	Glu	Gln	Lys	Leu	Ser	Arg	Ala	Lys	Thr	Gln	Ile	Asn	Ser
									1125					1130	1135
Gln	Leu	Arg	Pro	Met	Met	Ser	Glu	Leu	Glu	Glu	Arg	Ala	Arg	Gln	Gln
									1140					1145	1150
Arg	Gly	His	Leu	His	Leu	Leu	Glu	Thr	Ser	Ile	Asp	Gly	Ile	Leu	Ala
									1155					1160	1165
Asp	Val	Lys	Asn	Leu	Glu	Asn	Ile	Arg	Asp	Asn	Leu	Pro	Pro	Gly	Cys
									1170					1175	1180
Tyr	Asn	Thr	Gln	Ala	Leu	Glu	Gln	Gln							
									1185					1190	

(2) INFORMATION FOR SEQ ID NO:14:

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 118..3453
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(ix) FEATURE:
      (A) NAME/KEY: polyA_site
      (B) LOCATION: 4296
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACCACCTGA	TCGAAGGAAA	AGGAAGGCAC	AGCGGAGCGC	AGAGTGAGAA	CCACCAACCG	60
AGGCGCCGGG	CAGCGACCCC	TGCAGCGGAG	ACAGAGACTG	AGCGGCCCGG	CACCGCC	117
ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG	165					
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu						
1195 1200 1205 1210						
CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG	213					
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly						
1215 1220 1225						
AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT	261					
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly						
1230 1235 1240						
AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC	309					
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His						
1245 1250 1255						
TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC	357					
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg						
1260 1265 1270						
TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT	405					
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys						
1275 1280 1285 1290						
GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA	453					

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg	
1295 1300 1305	
TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC	501
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys	
1310 1315 1320	
ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT	549
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala	
1325 1330 1335	
GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT	597
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala	
1340 1345 1350	
GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG	645
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu	
1355 1360 1365 1370	
GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT	693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His	
1375 1380 1385	
TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC	741
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr	
1390 1395 1400	
TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT	789
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn	
1405 1410 1415	
GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT	837
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe	
1420 1425 1430	
AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA	885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys	
1435 1440 1445 1450	
TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC	933
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp	
1455 1460 1465	
TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC	981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile	
1470 1475 1480	
CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC	1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly	
1485 1490 1495	
AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT	1077
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn	
1500 1505 1510	
GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT	1125
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr	
1515 1520 1525 1530	
CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT	1173



Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr	
1535 1540 1545	
GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC	1221
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala	
1550 1555 1560	
CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT	1269
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys	
1565 1570 1575	
CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC	1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr	
1580 1585 1590	
AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT	1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys	
1595 1600 1605 1610	
AAC TGT CAA GGG GGA GGG GCC TGT GAT CCA GAC ACA GGA GAT TGT TAT	1413
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr	
1615 1620 1625	
TCA GGG GAT GAG AAT CCT GAC ATT GAG TGT GCT GAC TGC CCA ATT GGT	1461
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly	
1630 1635 1640	
TTC TAC AAC GAT CCG CAC GAC CCC CGC AGC TGC AAG CCA TGT CCC TGT	1509
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys	
1645 1650 1655	
CAT AAC GGG TTC AGC TGC TCA GTG ATT CCG GAG ACG GAG GAG GTG GTG	1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val	
1660 1665 1670	
TGC AAT AAC TGC CCT CCC GGG GTC ACC GGT GCC CGC TGT GAG CTC TGT	1605
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys	
1675 1680 1685 1690	
GCT GAT GGC TAC TTT GGG GAC CCC TTT GGT GAA CAT GGC CCA GTG AGG	1653
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg	
1695 1700 1705	
CCT TGT CAG CCC TGT CAA TGC AAC AGC AAT GTG GAC CCC AGT GCC TCT	1701
Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser	
1710 1715 1720	
GGG AAT TGT GAC CGG CTG ACA GGC AGG TGT TTG AAG TGT ATC CAC AAC	1749
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn	
1725 1730 1735	
ACA GCC GGC ATC TAC TGC GAC CAG TGC AAA GCA GGC TAC TTC GGG GAC	1797
Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp	
1740 1745 1750	
CCA TTG GCT CCC AAC CCA GCA GAC AAG TGT CGA GCT TGC AAC TGT AAC	1845
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn	
1755 1760 1765 1770	
CCC ATG GGC TCA GAG CCT GTA GGA TGT CGA AGT GAT GGC ACC TGT GTT	1893

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val	
1775 1780 1785	
TGC AAG CCA GGA TTT GGT GGC CCC AAC TGT GAG CAT GGA GCA TTC AGC	1941
Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser	
1790 1795 1800	
TGT CCA GCT TGC TAT AAT CAA GTG AAG ATT CAG ATG GAT CAG TTT ATG	1989
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met	
1805 1810 1815	
CAG CAG CTT CAG AGA ATG GAG GCC CTG ATT TCA AAG GCT CAG GGT GGT	2037
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly	
1820 1825 1830	
GAT GGA GTA GTA CCT GAT ACA GAG CTG GAA GGC AGG ATG CAG CAG GCT	2085
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala	
1835 1840 1845 1850	
GAG CAG GCC CTT CAG GAC ATT CTG AGA GAT GCC CAG ATT TCA GAA GGT	2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly	
1855 1860 1865	
GCT AGC AGA TCC CTT GGT CTC CAG TTG GCC AAG GTG AGG AGC CAA GAG	2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu	
1870 1875 1880	
AAC AGC TAC CAG AGC CGC CTG GAT GAC CTC AAG ATG ACT GTG GAA AGA	2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg	
1885 1890 1895	
GTT CGG GCT CTG GGA AGT CAG TAC CAG AAC CGA GTT CGG GAT ACT CAC	2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His	
1900 1905 1910	
AGG CTC ATC ACT CAG ATG CAG CTG AGC CTG GCA GAA AGT GAA GCT TCC	2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser	
1915 1920 1925 1930	
TTG GGA AAC ACT AAC ATT CCT GCC TCA GAC CAC TAC GTG GGG CCA AAT	2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn	
1935 1940 1945	
GGC TTT AAA AGT CTG GCT CAG GAG GCC ACA AGA TTA GCA GAA AGC CAC	2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His	
1950 1955 1960	
GTT GAG TCA GCC AGT AAC ATG GAG CAA CTG ACA AGG GAA ACT GAG GAC	2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp	
1965 1970 1975	
TAT TCC AAA CAA GCC CTC TCA CTG GTG CGC AAG GCC CTG CAT GAA GGA	2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly	
1980 1985 1990	
GTC GGA AGC GGA AGC GGT AGC CCG GAC GGT GCT GTG GTG CAA GGG CTT	2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu	
1995 2000 2005 2010	
GTG GAA AAA TTG GAG AAA ACC AAG TCC CTG GCC CAG CAG TTG ACA AGG	2613

Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg	
2015								2020				2025				
GAG	GCC	ACT	CAA	GCG	GAA	ATT	GAA	GCA	GAT	AGG	TCT	TAT	CAG	CAC	AGT	2661
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser	
2030				2035				2040								
CTC	CGC	CTC	CTG	GAT	TCA	GTG	TCT	CCG	CTT	CAG	GGA	GTC	AGT	GAT	CAG	2709
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Pro	Leu	Gln	Gly	Val	Ser	Asp	Gln	
2045				2050				2055								
TCC	TTT	CAG	GTG	GAA	GAA	GCA	AAG	AGG	ATC	AAA	CAA	AAA	GCG	GAT	TCA	2757
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser	
2060				2065				2070								
CTC	TCA	AGC	CTG	GTA	ACC	AGG	CAT	ATG	GAT	GAG	TTC	AAG	CGT	ACA	CAA	2805
Leu	Ser	Ser	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln	
2075				2080				2085				2090				
AAG	AAT	CTG	GGA	AAC	TGG	AAA	GAA	GAA	GCA	CAG	CAG	CTC	TTA	CAG	AAT	2853
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn	
2095				2100				2105								
GGA	AAA	AGT	GGG	AGA	GAG	AAA	TCA	GAT	CAG	CTG	CTT	TCC	CGT	GCC	AAT	2901
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn	
2110				2115				2120								
CTT	GCT	AAA	AGC	AGA	GCA	CAA	GAA	GCA	CTG	AGT	ATG	GGC	AAT	GCC	ACT	2949
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr	
2125				2130				2135								
TTT	TAT	GAA	GTT	GAG	AGC	ATC	CTT	AAA	AAC	CTC	AGA	GAG	TTT	GAC	CTG	2997
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu	
2140				2145				2150								
CAG	GTG	GAC	AAC	AGA	AAA	GCA	GAA	GCT	GAA	GAA	GCC	ATG	AAG	AGA	CTC	3045
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu	
2155				2160				2165				2170				
TCC	TAC	ATC	AGC	CAG	AAG	GTT	TCA	GAT	GCC	AGT	GAC	AAG	ACC	CAG	CAA	3093
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln	
2175				2180				2185								
GCA	GAA	AGA	GCC	CTG	GGG	AGC	GCT	GCT	GCT	GAT	GCA	CAG	AGG	GCA	AAG	3141
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys	
2190				2195				2200								
AAT	GGG	GCC	GGG	GAG	GCC	CTG	GAA	ATC	TCC	AGT	GAG	ATT	GAA	CAG	GAG	3189
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu	
2205				2210				2215								
ATT	GGG	AGT	CTG	AAC	TTG	GAA	GCC	AAT	GTG	ACA	GCA	GAT	GGA	GCC	TTG	3237
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu	
2220				2225				2230								
GCC	ATG	GAA	AAG	GGA	CTG	GCC	TCT	CTG	AAG	AGT	GAG	ATG	AGG	GAA	GTG	3285
Ala	Met	Glu	Lys	Gly	Leu	Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val	
2235				2240				2245				2250				
GAA	GGA	GAG	CTG	GAA	AGG	AAG	GAG	CTG	GAG	TTT	GAC	ACG	AAT	ATG	GAT	3333

Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp	
2255	2260 2265
GCA GTA CAG ATG GTG ATT ACA GAA GCC CAG AAG GTT GAT ACC AGA GCC	3381
Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala	
2270	2275 2280
AAG AAC GCT GGG GTT ACA ATC CAA GAC ACA CTC AAC ACA TTA GAC GGC	3429
Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly	
2285	2290 2295
CTC CTG CAT CTG ATG GGT ATG TGA ACCCACAACC CACAACCTTC CAGCTCCATG	3483
Leu Leu His Leu Met Gly Met *	
2300	2305
CTCCAGGGCT TTGCTCCAGA AACTCACTA TACCTAGCCC CAGCAAAGGG GAGTCTCAGC	3543
TTTCCTTAAG GATATCAGTA AATGTGCTTT GTTTCAGGC CCAGATAACT TTCGGCAGGT	3603
TCCCTTACAT TTAAGTGGACC CTGTTTTACC GTTGCTAAGA TGGGTCAGT AACACCTATT	3663
GCACTTGGGG GTAAAGGTCT GTGGGCCAAA GAACAGGTGT ATATAAGCAA CTTACAGAA	3723
CACGAGACAG CTTGGGAATC CTGCTAAAGA GTCTGGCCTG GACCCTGAGA AGCCAGTGGA	3783
CAGTTTTAAG CAGAGGAATA ACATCACCAC TGTATATTTT AGAAAGATCA CTAGGGCAGC	3843
CGAGTGGAGG AAAGCTTGAA GAGGGGGTTA GAGAGAAGGC AGGTTGAGAC TACTTAAGAT	3903
ATTGTTGAAA TAATTGAAGA GAGAAATGAC AGGAGCCTGC TCTAAGGCAG TAGAATGGTG	3963
GCTGGGAAGA TGTGAAGGAA GATTTTCCCA GTCTGTGAAG TCAAGAATCA CTTGCCGGCC	4023
GGGTGTGGTG GCTCAGCCT GTAATTCTAG CACTTTGGGA GACTGAAGCG GGTGGATCAC	4083
CCGAGGTCAG GAGTTGAAGA CCAGCCTGGC CAACATGGTG AAACCCTGTC TCTACTAAAA	4143
GTACAAAAAT TAGCTGGATG ATGGTGGTGG GCGCCTGTAA TTCCAGCTAC TCAGGAGTCT	4203
GAGGCAGGAG AATCGCTTGA ACCCAGGAGG CGAGGTTACA GTGAGCCAAG ATTGCACCAC	4263
TGCTCTTCCA GCCTGGGAAC AGAGAGACTG CCTAAAAAAA AAAAAAAAAA AAA	4316

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu	
1 5 10 15	
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly	
20 25 30	

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly  
 35 40 45  
 Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His  
 50 55 60  
 Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg  
 65 70 75 80  
 Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys  
 85 90 95  
 Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg  
 100 105 110  
 Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys  
 115 120 125  
 Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala  
 130 135 140  
 Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala  
 145 150 155 160  
 Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu  
 165 170 175  
 Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His  
 180 185 190  
 Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr  
 195 200 205  
 Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn  
 210 215 220  
 Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe  
 225 230 235 240  
 Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys  
 245 250 255  
 Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp  
 260 265 270  
 Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile  
 275 280 285  
 Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly  
 290 295 300  
 Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn  
 305 310 315 320  
 Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr  
 325 330 335  
 Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr  
 340 345 350

Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala  
 355 360 365

Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys  
 370 375 380

Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr  
 385 390 395 400

Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys  
 405 410 415

Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr  
 420 425 430

Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly  
 435 440 445

Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys  
 450 455 460

His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val  
 465 470 475 480

Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys  
 485 490 495

Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg  
 500 505 510

Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser  
 515 520 525

Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn  
 530 535 540

Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp  
 545 550 555 560

Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn  
 565 570 575

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val  
 580 585 590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser  
 595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met  
 610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly  
 625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala  
 645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly  
 660 665 670

Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu	675	680	685	
Asn	Ser	Tyr	Gln	Ser	Arg	Leu	Asp	Asp	Leu	Lys	Met	Thr	Val	Glu	Arg	690	695	700	
Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Arg	Val	Arg	Asp	Thr	His	705	710	715	720
Arg	Leu	Ile	Thr	Gln	Met	Gln	Leu	Ser	Leu	Ala	Glu	Ser	Glu	Ala	Ser	725	730	735	
Leu	Gly	Asn	Thr	Asn	Ile	Pro	Ala	Ser	Asp	His	Tyr	Val	Gly	Pro	Asn	740	745	750	
Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Leu	Ala	Glu	Ser	His	755	760	765	
Val	Glu	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Thr	Arg	Glu	Thr	Glu	Asp	770	775	780	
Tyr	Ser	Lys	Gln	Ala	Leu	Ser	Leu	Val	Arg	Lys	Ala	Leu	His	Glu	Gly	785	790	795	800
Val	Gly	Ser	Gly	Ser	Gly	Ser	Pro	Asp	Gly	Ala	Val	Val	Gln	Gly	Leu	805	810	815	
Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg	820	825	830	
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser	835	840	845	
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Pro	Leu	Gln	Gly	Val	Ser	Asp	Gln	850	855	860	
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser	865	870	875	880
Leu	Ser	Ser	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln	885	890	895	
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn	900	905	910	
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn	915	920	925	
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr	930	935	940	
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu	945	950	955	960
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu	965	970	975	
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln	980	985	990	

Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys
	995						1000					1005			
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu
	1010					1015					1020				
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu
	1025				1030					1035					1040
Ala	Met	Glu	Lys	Gly	Leu	Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val
			1045						1050					1055	
Glu	Gly	Glu	Leu	Glu	Arg	Lys	Glu	Leu	Glu	Phe	Asp	Thr	Asn	Met	Asp
			1060					1065					1070		
Ala	Val	Gln	Met	Val	Ile	Thr	Glu	Ala	Gln	Lys	Val	Asp	Thr	Arg	Ala
		1075					1080						1085		
Lys	Asn	Ala	Gly	Val	Thr	Ile	Gln	Asp	Thr	Leu	Asn	Thr	Leu	Asp	Gly
	1090					1095					1100				
Leu	Leu	His	Leu	Met	Gly	Met									
	1105				1110										

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligomer primers"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCGCAGAG TGAGAACCAC

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligomer primers"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTGTATTCT GCAGAGCTGC

20



(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCCTTTCCCTACCTTGTG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTGGAAGCCTGGCAGACAT

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Gly Thr Cys Thr Thr Thr Ala Thr Ala Gly Gly Gly Ala Gly Gly  
1 5 10 15  
Thr Thr Gly Gly Cys Cys Ala Gly Thr Cys Ala Ala Thr Ala Gly Gly  
20 25 30  
Thr Thr Ala Cys Thr Thr Thr Ala Thr Gly Ala Gly Thr Thr Gly Cys  
35 40 45  
Thr Ala Ala Cys Cys Cys Thr Gly Gly Thr Gly Ala Gly Cys Ala Gly  
50 55 60  
Gly Ala Ala Gly Thr Thr Ala Thr Gly Thr Gly Gly Ala Cys Cys Ala  
65 70 75 80  
Gly Gly Ala Gly Ala Gly Ala Ala Ala Cys Cys Cys Thr Thr Gly Gly  
85 90 95

Thr Thr Cys Ala Gly Cys Cys Thr Gly Gly Ala Gly Ala Ala Ala Gly  
 100 105 110  
 Gly Ala Gly Ala Gly Gly Thr Thr Gly Ala Cys Cys Cys Thr Ala Ala  
 115 120 125  
 Ala Cys Thr Gly Gly Ala Gly Gly Gly Thr Gly Gly Ala Gly Ala Gly  
 130 135 140  
 Gly Ala Cys Cys Cys Thr Gly Thr Thr Gly Thr Gly Ala Cys Thr Cys  
 145 150 155 160  
 Thr Cys Cys Gly Ala Cys Thr Gly Ala Cys Thr Thr Gly Thr Cys Thr  
 165 170 175  
 Thr Cys Cys Thr Thr Gly Ala Thr Gly Thr Cys Cys Thr Thr Thr Ala  
 180 185 190  
 Ala Gly Cys Cys Gly Gly Ala Gly Cys Thr Gly Ala Thr Thr Cys Gly  
 195 200 205  
 Gly Gly Cys Thr Gly Cys Thr Gly Cys Cys Thr Thr Ala Thr Thr Thr  
 210 215 220  
 Cys Thr Gly Ala Gly Thr Thr Ala Gly Cys Gly Cys Thr Cys Thr Thr  
 225 230 235 240  
 Ala Ala Gly Ala Thr Thr Gly Gly Gly Cys Cys Thr Cys Cys Cys Ala  
 245 250 255  
 Gly Thr Thr Thr Gly Ala Gly Gly Ala Ala Gly Gly Gly Gly Cys Gly  
 260 265 270  
 Gly Gly Cys Thr Gly Cys Thr Gly Thr Cys Thr Ala Cys Cys Thr Cys  
 275 280 285  
 Thr Gly Thr Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly  
 290 295 300  
 Ala Cys Cys Ala Cys Cys Cys Cys Gly Gly Gly Ala Gly Ala Gly Ala  
 305 310 315 320  
 Ala Gly Gly Ala Gly Gly Gly Cys Thr Cys Cys Gly Gly Gly Gly Ala  
 325 330 335  
 Ala Thr Cys Thr Cys Gly Cys Ala Cys Ala Thr Thr Cys Cys Ala Gly  
 340 345 350  
 Gly Cys Ala Ala Ala Gly Gly Cys Thr Cys Cys Cys Gly Gly Gly Cys  
 355 360 365  
 Cys Gly Cys Ala Gly Cys Cys Thr Cys Thr Gly Thr Gly Cys Cys Ala  
 370 375 380  
 Cys Ala Cys Cys Cys Thr Thr Gly Gly Cys Cys Cys Gly Gly Gly Cys  
 385 390 395 400  
 Cys Ala Gly Gly Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Cys Cys  
 405 410 415

Thr Cys Gly Cys Thr Gly Cys Gly Ala Gly Gly Gly Gly Gly Ala Gly  
 420 425 430  
 Cys Gly Gly Gly Cys Gly Gly Cys Thr Gly Cys Gly Gly Gly Gly Ala  
 435 440 445  
 Gly Cys Gly Ala Thr Thr Thr Thr Cys Cys Ala Gly Cys Cys Cys Gly  
 450 455 460  
 Gly Thr Thr Thr Gly Thr Gly Cys Thr Cys Thr Gly Thr Gly Thr Gly  
 465 470 475 480  
 Thr Thr Thr Gly Thr Cys Thr Gly Cys Cys Thr Cys Thr Gly Gly Ala  
 485 490 495  
 Gly Gly Gly Cys Thr Gly Gly Gly Thr Cys Cys Thr Cys Cys Thr Thr  
 500 505 510  
 Ala Thr Thr Cys Ala Cys Ala Gly Gly Thr Gly Ala Gly Thr Cys Ala  
 515 520 525  
 Cys Ala Cys Cys Cys Thr Gly Ala Ala Ala Cys Ala Cys Ala Gly Gly  
 530 535 540  
 Cys Thr Cys Thr Cys Thr Thr Cys Cys Thr Gly Thr Cys Ala Gly Gly  
 545 550 555 560  
 Ala Cys Thr Gly Ala Gly Thr Cys Ala Gly Gly Thr Ala Gly Ala Ala  
 565 570 575  
 Gly Ala Gly Thr Cys Gly Ala Thr Ala Ala Ala Ala Cys Cys Ala Cys  
 580 585 590  
 Cys Thr Gly Ala Thr Cys Ala Ala Gly Gly Ala Ala Ala Gly Gly  
 595 600 605  
 Ala Ala Gly Gly Cys Ala Cys Ala Gly Cys Gly Gly Ala Gly Cys Gly  
 610 615 620  
 Cys Ala Gly Ala Gly Thr Gly Ala Gly Ala Ala Cys Cys Ala Cys Cys  
 625 630 635 640  
 Ala Ala Cys Cys Gly Ala Gly Gly Cys Gly Cys Cys Gly Gly Gly Cys  
 645 650 655  
 Ala Gly Cys Gly Ala Cys Cys Cys Cys Thr Gly Cys Ala Gly Cys Gly  
 660 665 670  
 Gly Ala Gly Ala Cys Ala Gly Ala Gly Ala Cys Thr Gly Ala Gly Cys  
 675 680 685  
 Gly Gly Cys Cys Cys Gly Gly Cys Ala Cys Cys Gly Cys Cys Ala Thr  
 690 695 700  
 Gly Cys Cys Thr Gly Cys Gly Cys Thr Cys Thr Gly Gly Cys Thr Gly  
 705 710 715 720